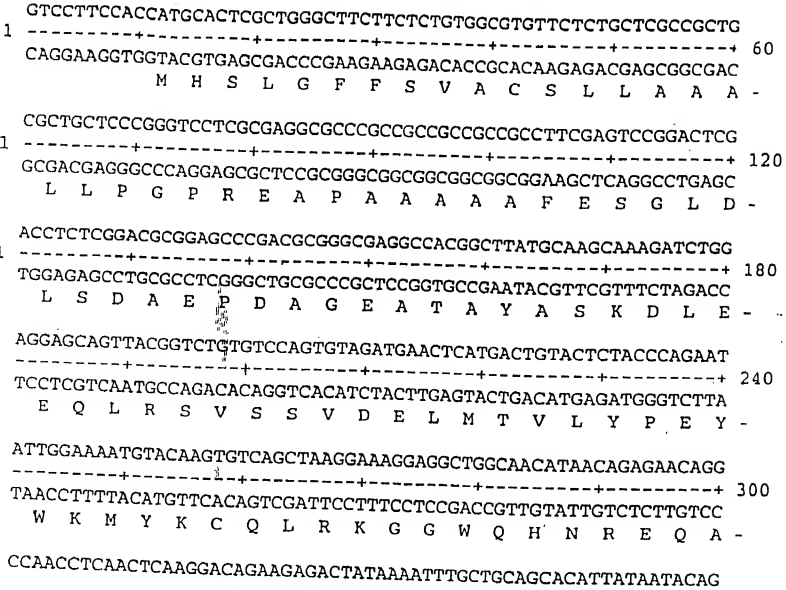
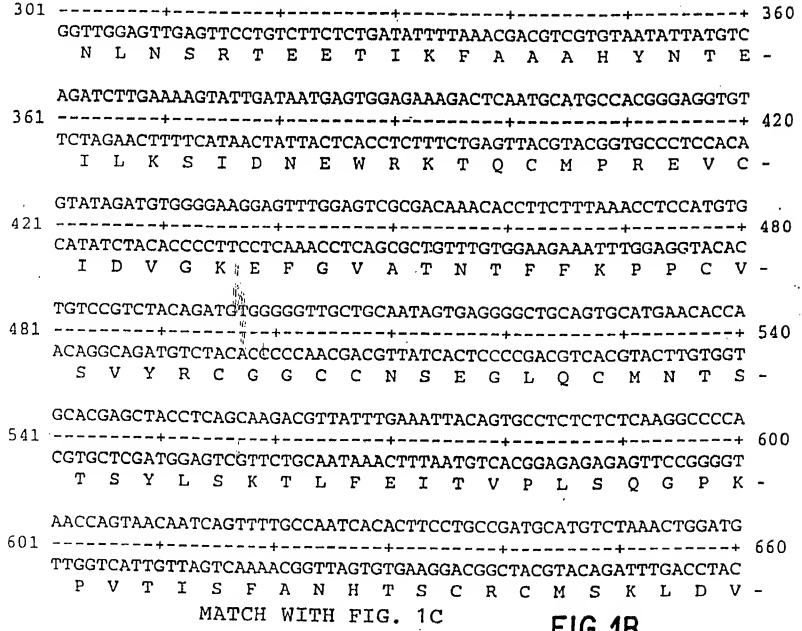


MATCH WITH FIG. 1B

FIG. 1A

MATCH WITH FIG. 1A



MATCH WITH FIG. 1C

FIG. 1B

MATCH WITH FIG. 1B

```
     TTTACAGACAAGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTC
661  ---------+---------+---------+---------+---------+---------+ 720
     AAATGTCTGTTCAAGTAAGGTAATAATCTGCAAGGGACGGTCGTTGTGATGGTGTCACAG
       Y  R  Q  V  H  S  I  I  R  R  S  L  P  A  T  L  P  Q  C  Q -

     AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC
721  ---------+---------+---------+---------+---------+---------+ 780
     TCCGTCGCTTGTTCTGGACGGGGTGGTTAATGTACACCTTATTAGTGTAGACGTCTACGG
       A  A  N  K  T  C  P  T  N  Y  M  W  N  N  H  I  C  R  C  L -

     TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC
781  ---------+---------+---------+---------+---------+---------+ 840
     ACCGAGTCCTTCTAAAATACAAAAGGAGCCTACGACCTCTACTGAGTTGTCTACCTAAGG
       A  Q  E  D  F  M  F  S  S  D  A  G  D  D  S  T  D  G  F  H -

     ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAGACCTGTCAGTGTGTCTGCAGAG
841  ---------+---------+---------+---------+---------+---------+ 900
     TACTGTAGACACCTGGTTTGTTCCTCGACCTACTTCTCTGGACAGTCACACAGACGTCTC
       D  I  C  G  P  N  K  E  L  D  E  E  T  C  Q  C  V  C  R  A -

     CGGGGCTTCGGCCTGCCAGCTGTGGACCCCACAAAGAACTAGACAGAAACTCATGCCAGT
901  ---------+---------+---------+---------+---------+---------+ 960
     GCCCCGAAGCCGGACGGTCGACACCTGGGGTGTTTCTTGATCTGTCTTTGAGTACGGTCA
       G  L  R  P  A  S  C  G  P  H  K  E  L  D  R  N  S  C  Q  C -

     GTGTCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGCCAACCGAGAATTTGATGAAA
961  ---------+---------+---------+---------+---------+---------+ 1020
     CACAGACATTTTTGTTTGAGAAGGGGTCGGTTACACCCCGGTTGGCTCTTAAACTACTTT
```

MATCH WITH FIG. 1D

FIG. 1C

MATCH WITH FIG. 1C

```
      V  C  K  N  K  L  F  P  S  Q  C  G  A  N  R  E  F  D  E  N -

      ACACATGCCAGTGTGTATGTAAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAA
1021  ---------+---------+---------+---------+---------+---------+ 1080
      TGTGTACGGTCACACATACATTTTCTTGGACGGGGTCTTTAGTTGGGGATTTAGGACCTT
        T  C  Q  C  V  C  K  R  T  C  P  R  N  Q  P  L  N  P  G  K -

      AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGAAGTTCC
1081  ---------+---------+---------+---------+---------+---------+ 1140
      TTACACGGACACTTACATGTCTTTCAGGTGTCTTTACGAACAATTTTCCTTTCTTCAAGG
        C  A  C  E  C  T  E  S  P  Q  K  C  L  L  K  G  K  K  F  H -

      ACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAGAAGGCTTGTGAGC
1141  ---------+---------+---------+---------+---------+---------+ 1200
      TGGTGGTTTGTACGTCGACAATGTCTGCCGGTACATGCTTGGCGGTCTTCCGAACACTCG
        H  Q  T  C  S  C  Y  R  R  P  C  T  N  R  Q  K  A  C  E  P -

      CAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCCTTCATATTGGCAAAGACCAC
1201  ---------+---------+---------+---------+---------+---------+ 1260
      GTCCTAAAAGTATATCACTTCTTCACACAGCAACACAGGGAAGTATAACCGTTTCTGGTG
        G  F  S  Y  S  E  E  V  C  R  C  V  P  S  Y  W  Q  R  P  Q -

      AAATGAGCTAAGATTGTACTGTTTTCCAGTTCATCGATTTTCTATTATGGAAAACTGTGT
```

MATCH WITH FIG. 1E

FIG. 1D

MATCH WITH FIG. 1D

```
1261 ---------+---------+---------+---------+---------+---------+ 1320
     TTTACTCGATTCTAACATGACAAAAGGTCAAGTAGCTAAAAGATAATACCTTTTGACACA
       M  S  *

     TGCCACAGTAGAACTGTCTGTGAACAGAGAGACCCTTGTGGGTCCATGCTAACAAAGACA
1321 ---------+---------+---------+---------+---------+---------+ 1380
     ACGGTGTCATCTTGACAGACACTTGTCTCTCTGGGAACACCCAGGTACGATTGTTTCTGT

     AAAGTCTGTCTTTCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGCTCATCTG
1381 ---------+---------+---------+---------+---------+---------+ 1440
     TTTCAGACAGAAAGGACTTGGTACACCTATTGAAATGTCTTTACCTGACCTCGAGTAGAC

     CAAAAGGCCTCTTGTAAAGACTGGTTTTCTGCCAATGACCAAACAGCCAAGATTTTCCTC
1441 ---------+---------+---------+---------+---------+---------+ 1500
     GTTTTCCGGAGAACATTTCTGACCAAAAGACGGTTACTGGTTTGTCGGTTCTAAAAGGAG

     TTGTGATTTCTTTAAAAGAATGACTATATAATTTATTTCCACTAAAAATATTGTTTCTGC
1501 ---------+---------+---------+---------+---------+---------+ 1560
     AACACTAAAGAAATTTTCTTACTGATATATTAAATAAAGGTGATTTTTATAACAAAGACG

     ATTCATTTTTATAGCAACAACAATTGGTAAAACTCACTGTGATCAATATTTTTATATCAT
1561 ---------+---------+---------+---------+---------+---------+ 1620
     TAAGTAAAAATATCGTTGTTGTTAACCATTTTGAGTGACACTAGTTATAAAAATATAGTA

     GCAAAATATGTTTAAAATAAAATGAAAATTGTATTTATAAAAAAAAAAAAAAA
1621 ---------+---------+---------+---------+---------+---- 1674
     CGTTTTATACAAATTTTATTTTACTTTTAACATAAATATTTTTTTTTTTTTTT
```

FIG. 1E

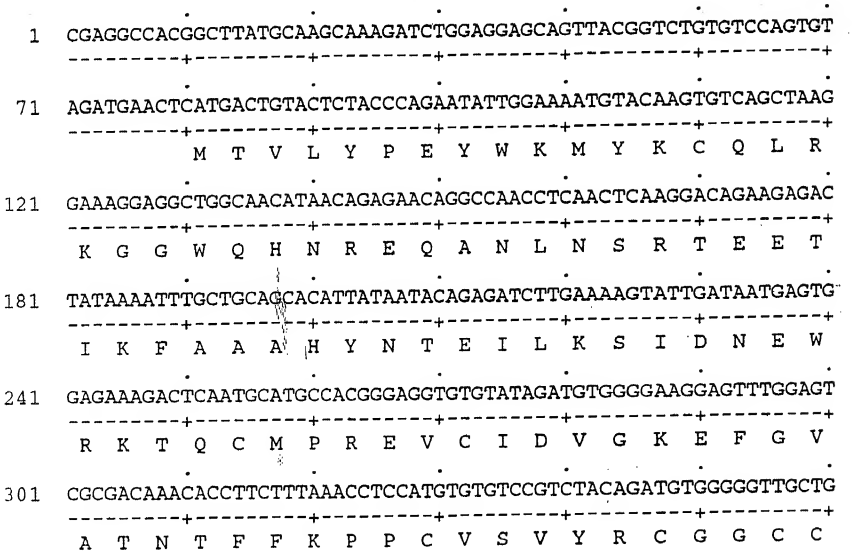


FIG. 2A

```
361 CAATAGTGAGGGGCTGCAGTGCATGAACACCAGCACGAGCTACCTCAGCAAGACGTTATT
    N  S  E  G  L  Q  C  M  N  T  S  T  S  Y  L  S  K  T  L  F

421 TGAAATTACAGTGCCTCTCTCTCAAGGCCCCAAACCAGTAACAATCAGTTTTGCCAATCA
    E  I  T  V  P  L  S  Q  G  P  K  P  V  T  I  S  F  A  N  H

481 CACTTCCTGCCGATGCATGTCTAAACTGGATGTTTACAGACAAGTTCATTCCATTATTAG
    T  S  C  R  C  M  S  K  L  D  V  Y  R  Q  V  H  S  I  I  R

541 ACGTTCCCTGCCAGCAACACTACCACAGTGTCAGGCAGCGAACAAGACCTGCCCCACCAA
    R  S  L  P  A  T  L  P  Q  C  Q  A  A  N  K  T  C  P  T  N

601 TTACATGTGGAATAATCACATCTGCAGATGCCTGGCTCAGGAAGATTTTATGTTTTCCTC
    Y  M  W  N  N  H  I  C  R  C  L  A  Q  E  D  F  M  F  S  S

661 GGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAAACAAGGAGCT
    D  A  G  D  D  S  T  D  G  F  H  D  I  C  G  P  N  K  E  L
```

FIG. 2B

FIG. 2C

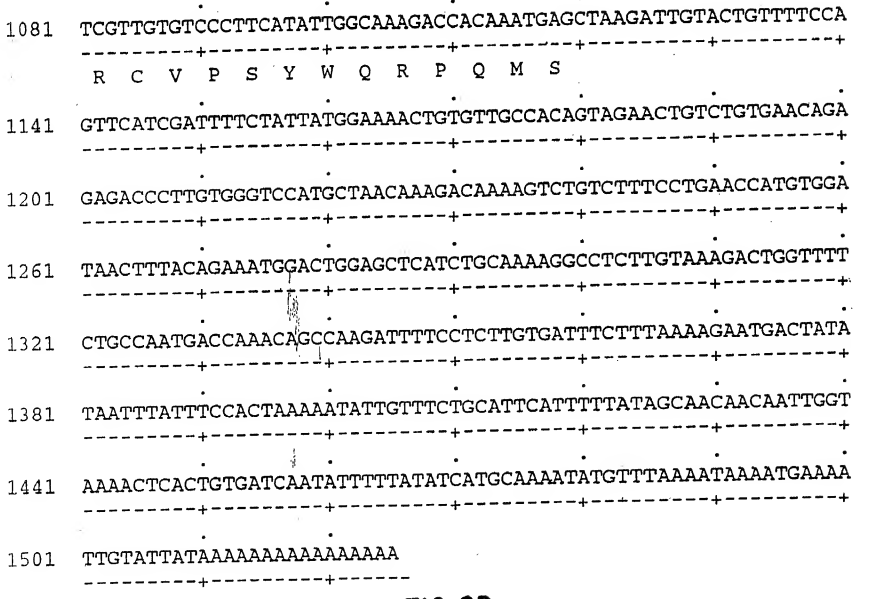


FIG. 2D

```
         1                                                    50
Pdgfa  .MRTLACLLL LGCGYLAHVL AEEAEIPREV IERLARSQIH SIRDLQRLLE
Pdgfb  MNRCWA.LFL SLCCYLRLVS AEGDPIPEEL YEMLSDHSIR SFDDLQRLLH
 Vegf  .....MNFLL SWVHWSLALL LY........ .......... .LHHAKWSQA
Vegf2  .......MTV LYPEYWKMYK CQ........ .......... .LRKGGWQHN

         51                                                  100
Pdgfa  IDSVGSEDSL DTSLRAHGVH ATKHVPEKRP LPIRRKRSI. .....EEAVP
Pdgfb  GDP.GEEDGA ELDLNMTRSH SGGELES... .LARGRRSLG SLTIAEPAMI
 Vegf  APMAE..... ......GGGQ NHHEVVKFMD .VYQR..... ..........
Vegf2  REQANLNSRT EETIKFAAAH YNTEILKSID NEWRK..... ..........

         101                                                 150
Pdgfa  AVCKTRTVIY EIPRSQVDPT SANFLIWPPC VEVKRCTGCC NTSSVKCQPS
Pdgfb  AECKTRTEVF EISRRLIDRT NANFLVWPPC VEVQRCSGCC NNRNVQCRPT
 Vegf  SYCHPIETLV DIFQEYPDEI ..EYIFKPSC VPLMRCGGCC NDEGLECVPT
Vegf2  TQCMPREVCI DVGKEFGVAT ..NTFFKPPC VSVYRCGGCC NSEGLQCMNT

         151                                                 200
Pdgfa  RVHHRSVKVA KVEYVRKKPK LKEVQVRLEE HLECAC.... AT........
Pdgfb  QVQLRPVQVR KIEIVRKKPI FKKATVTLED HLACKC.... ETVAAARPVT
 Vegf  EESNITMQIM RIK.PH..QG QHIGEMSFLQ HNKCECRPKK DRARQEKKSV
Vegf2  STSYLSKTLF EIT.VPLSQG PKPVTISFAN HTSCRCMSKL DVYRQVHSII
```

FIG. 3A

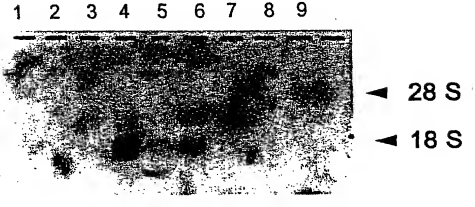
```
       201                                                 250
Pdgfa  ....TSLNPD YREEDTDVR. .......... .......... ..........
Pdgfb  RSPGGSQEQR AKTPQTRVTI RTVRVRRPPK GKHRKFKHTH DKTALKETLG
 Vegf  RGK....... .GKGQKRKRK KSRYKSWSVY VGARCCLMPW SLPGPHP...
Vegf2  RRSLPATLPQ CQAANKTCPT NYMWNNHICR CLAQEDFMFS SDAGDDSTDG

       251                                                 300
Pdgfa  .......... .......... .......... .......... ..........
Pdgfb  A......... .......... .......... .......... ..........
 Vegf  ....CGP... .......... .......CSE RRKHLFVQDP QTCKCSCKNT
Vegf2  FHDICGPNKE LDEETCQCVC RAGLRPASCG PHKEL...DR NSCQCVCKNK

       301                                                 350
Pdgfa  .......... .......... .......... .......... ..........
Pdgfb  .......... .......... .......... .......... ..........
 Vegf  ..DSRCKARQ LELNERTCRC DKPRR..... .......... ..........
Vegf2  LFPSQCGANR .EFDENTCQC VCKRTCPRNQ PLNPGKCACE CTESPQKCLL

       351                                               398
Pdgfa  .......... .......... .......... .......... ........
Pdgfb  .......... .......... .......... .......... ........
 Vegf  .......... .......... .......... .......... ........
Vegf2  KGKKFHHQTC SCYRRPCTNR QKACEPGFSY SEEVCRCVPS YWQRPQMS
```

FIG. 3B

PERCENTAGE (%) OF AMINO ACID IDENTITIES BETWEEN EACH PAIR OF GENES IS SHOWN IN THE FOLLWING TABLE				
	PDGFα	PDGFβ	VEGF	VEGF2
PDGFα				
PDGFβ	48.0			
VEGF	20.7	22.7		
VEGF2	23.5	22.4	30.0	

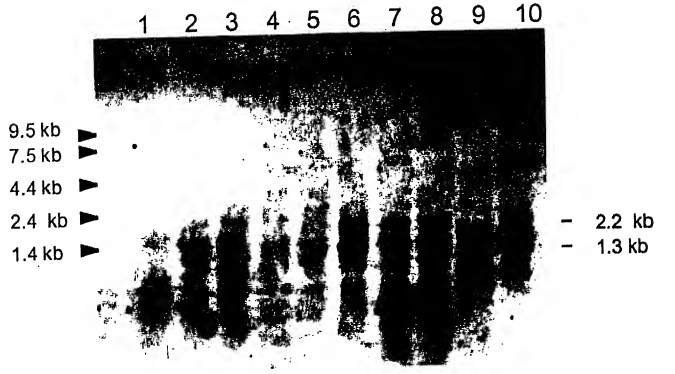
FIG.4

Expression of VEGF2 mRNA in Human Breast Tumor Cells



Lane 1. normal breast tissue
Lane 2. breast tumor tissue
Lane 3-9. breast tumor cell lines.

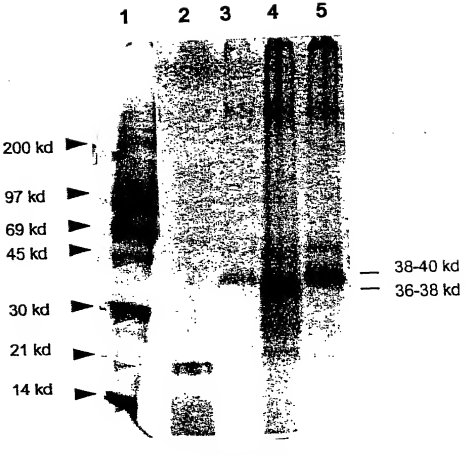
FIG.5



1. ovary
2. testes
3. gall bladder
4. kidney
5. liver
6. lung
7. spleen
8. prostate
9. Hippocampus
10. heart

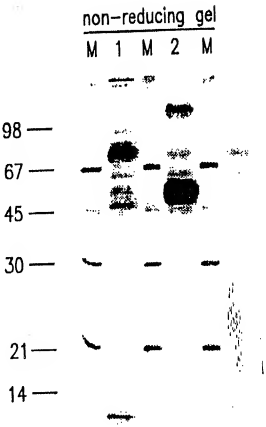
Expression of VEGF2 mRNA in human adult tissues.

FIG.6



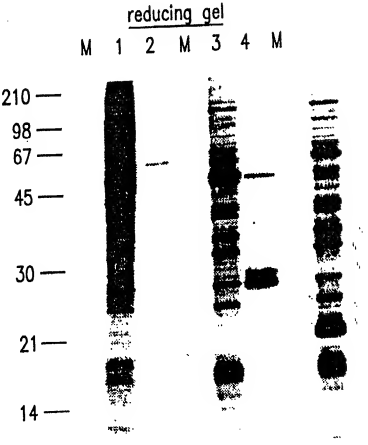
Lane 1: ^{14}C and rainbow M.W. marker
Lane 2: FGF control
Lane 3: VEGF2 (M13-reverse $ forward primers)
Lane 4: VEGF2 (M13-reverse & VEGF-F4 primers)
Lane 5: VEGF2 (M13-reverse & VEGF-F5 primers)

FIG.7



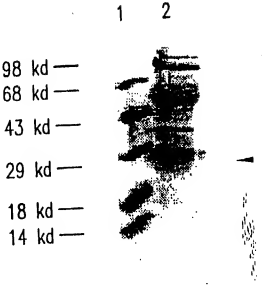
Lane M Marker
Lane 1 vector medium
Lane 2 VEGF2 medium

FIG.8A



Lane M: Marker
Lane 1: vector Cytoplasm
Lane 2: vector medium
Lane 3: VEGF2 Cytoplasm
Lane 4: VEGF2 medium

FIG.8B



Lane 1: Molelular weight marker
Lane 2: Precipitates containing VEGF2.

FIG.9

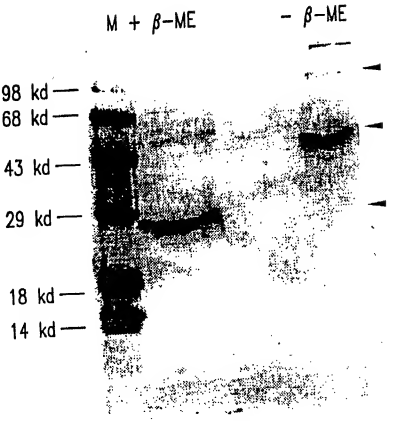


FIG.10

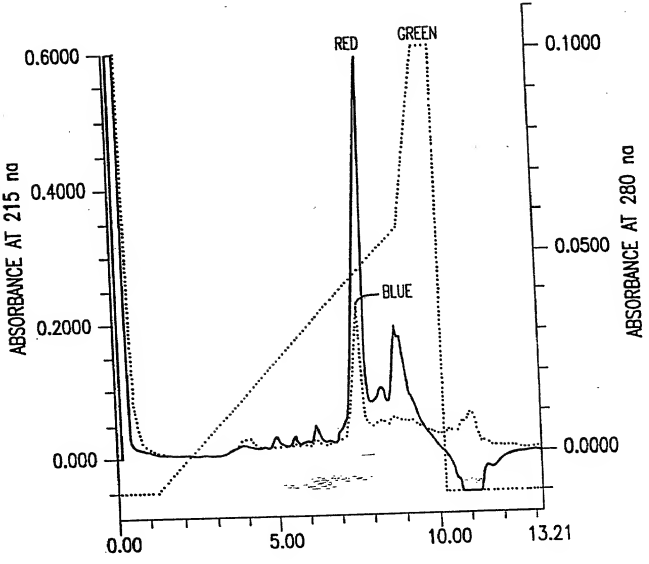

RED
GREEN
BLUE
0.6000
0.4000
0.2000
0.000
0.1000
0.0500
0.0000
ABSORBANCE AT 215 nm
ABSORBANCE AT 280 nm
0.00
5.00
10.00
13.21

FIG. 11

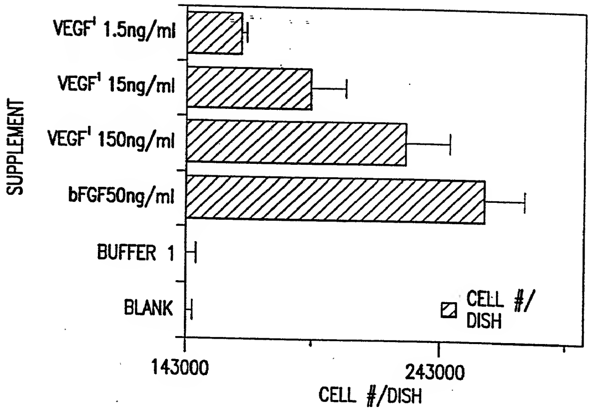

VEGF[1] 1.5ng/ml
VEGF[1] 15ng/ml
VEGF[1] 150ng/ml
bFGF50ng/ml
BUFFER 1
BLANK
SUPPLEMENT
CELL #/ DISH
143000
243000
CELL #/DISH

FIG.12

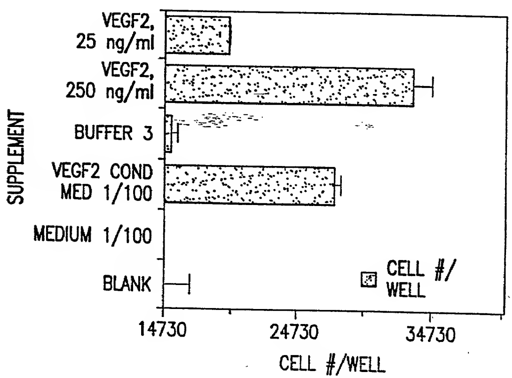

VEGF2, 25 ng/ml
VEGF2, 250 ng/ml
BUFFER 3
VEGF2 COND MED 1/100
MEDIUM 1/100
BLANK
SUPPLEMENT
CELL #/ WELL
14730
24730
34730
CELL #/WELL

FIG.13

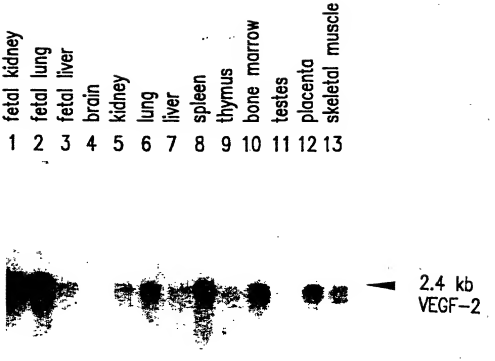


FIG.14A

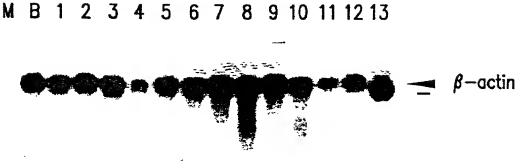
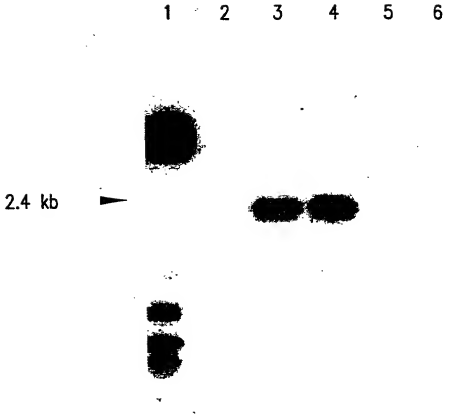
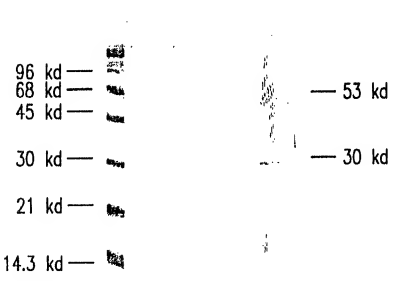


FIG.14B



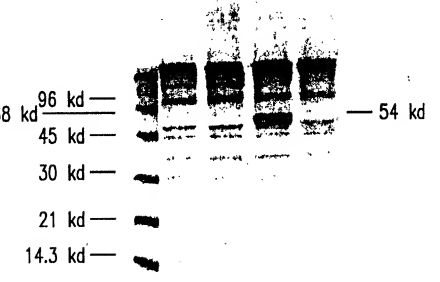
1. Molecular Weight Marker
2. umbelical vein endothelial cells
3. aortic smooth muscle cells
4. Dermal fibroblast

FIG.15



conditioned medium

FIG.16A



cell lysate

FIG.16B

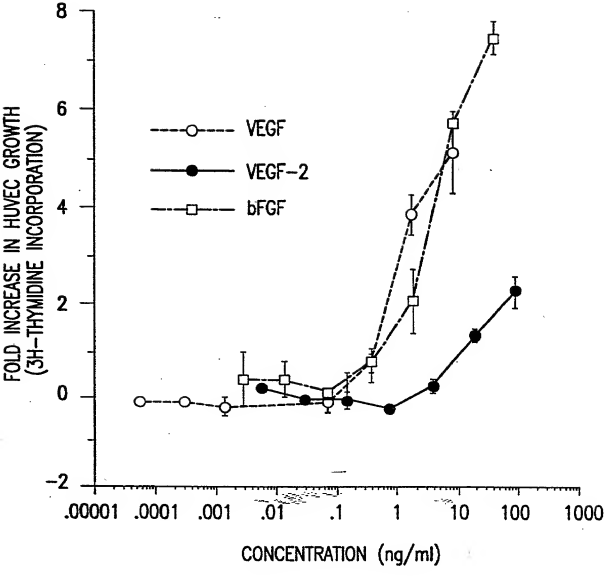

8
6
4
2
0
−2
FOLD INCREASE IN HUVEC GROWTH
(3H−THYMIDINE INCORPORATION)
VEGF
VEGF−2
bFGF
.00001
.0001
.001
.01
.1
1
10
100
1000
CONCENTRATION (ng/ml)

FIG.17

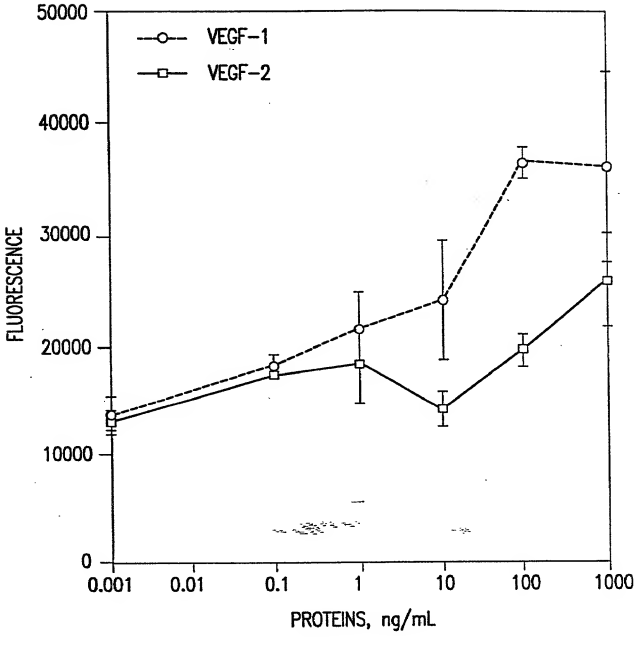

50000
40000
30000
20000
10000
0
FLUORESCENCE
VEGF-1
VEGF-2
0.001
0.01
0.1
1
10
100
1000
PROTEINS, ng/mL

FIG.18

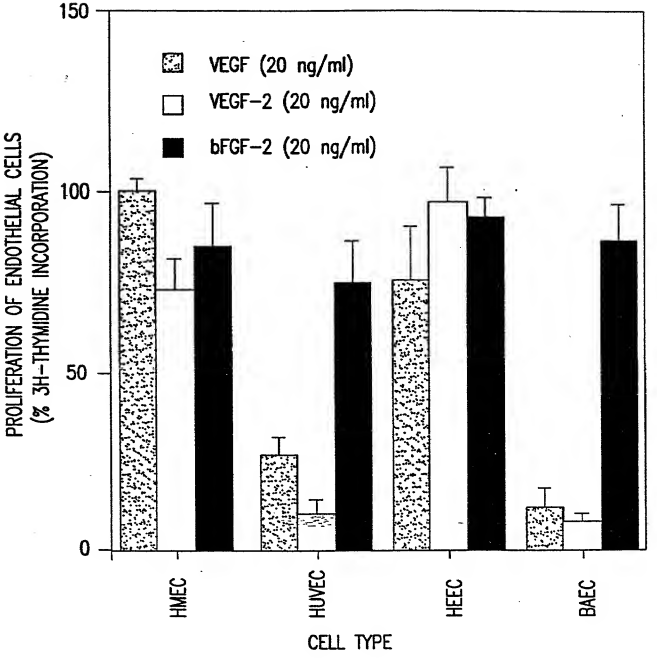

150
100
50
0
VEGF (20 ng/ml)
VEGF-2 (20 ng/ml)
bFGF-2 (20 ng/ml)
PROLIFERATION OF ENDOTHELIAL CELLS
(% 3H-THYMIDINE INCORPORATION)
HMEC
HUVEC
HEEC
BAEC
CELL TYPE

FIG.19

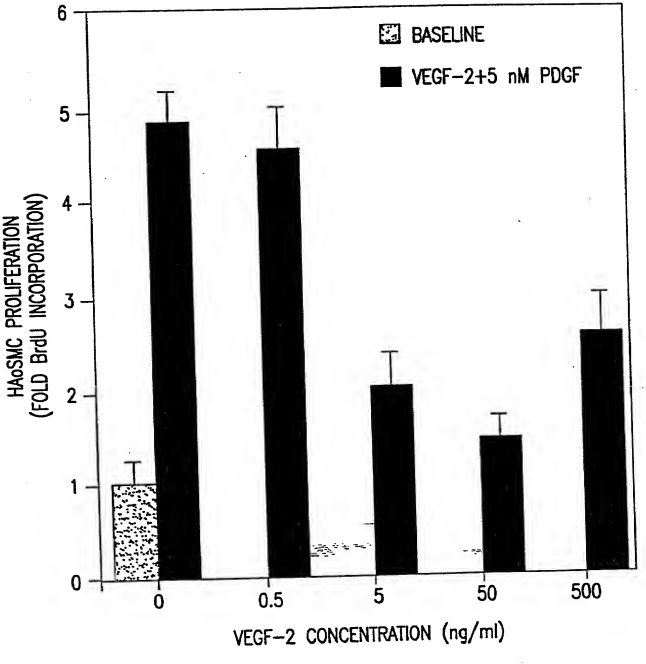

BASELINE
VEGF-2+5 nM PDGF
HAoSMC PROLIFERATION
(FOLD BrdU INCORPORATION)
0
1
2
3
4
5
6
0
0.5
5
50
500
VEGF-2 CONCENTRATION (ng/ml)

FIG.20A

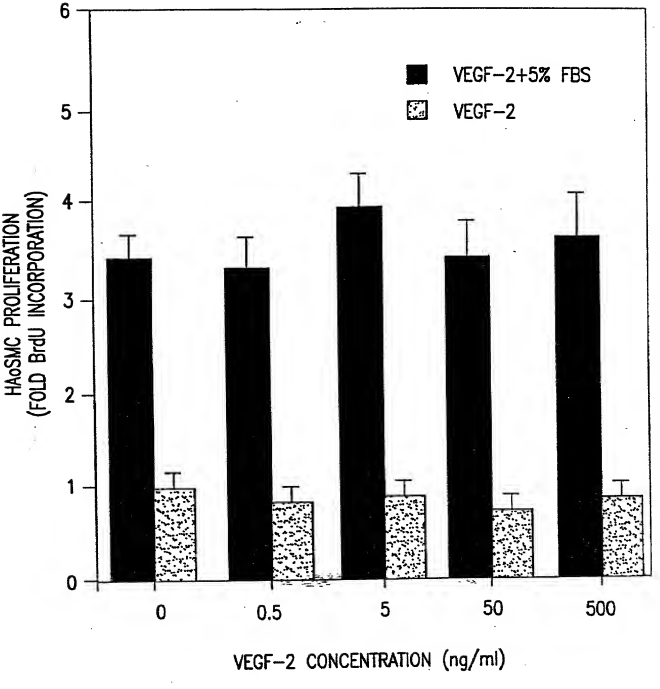

6
5
4
3
2
1
0
VEGF-2+5% FBS
VEGF-2
HAoSMC PROLIFERATION
(FOLD BrdU INCORPORATION)
0
0.5
5
50
500
VEGF-2 CONCENTRATION (ng/ml)

FIG.20B

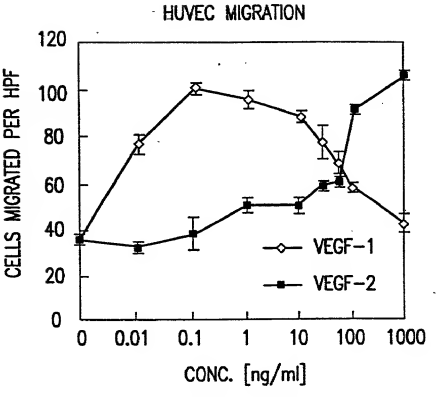


FIG.21A

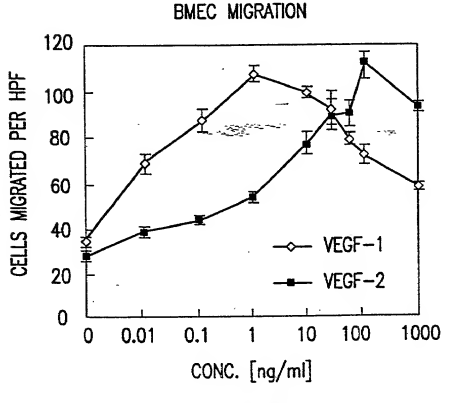


FIG.21B

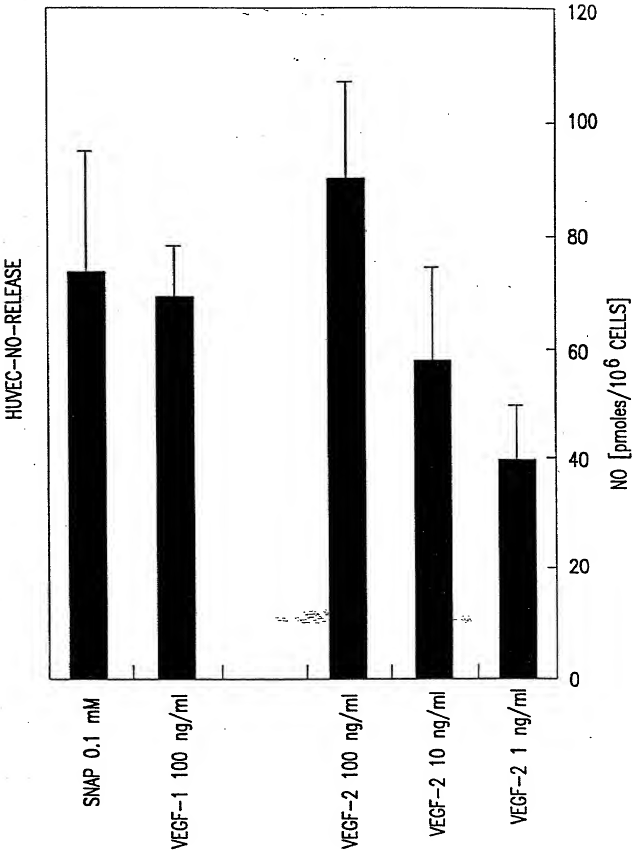

HUVEC-NO-RELEASE
NO [pmoles/10^6 CELLS]
120
100
80
60
40
20
0
SNAP 0.1 mM
VEGF-1 100 ng/ml
VEGF-2 100 ng/ml
VEGF-2 10 ng/ml
VEGF-2 1 ng/ml

FIG.22

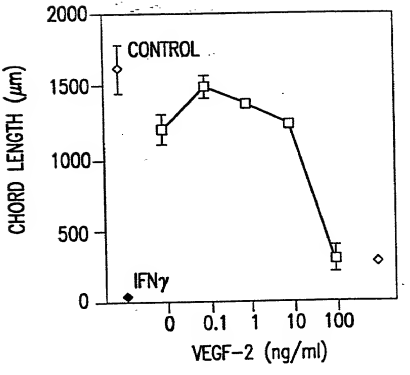


FIG.23

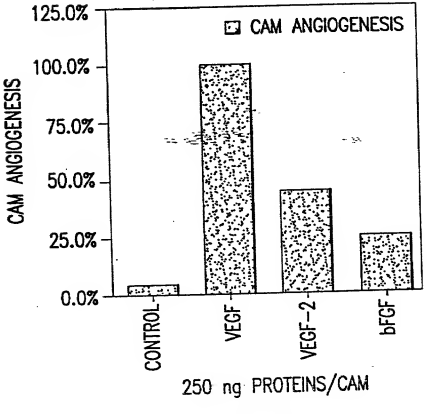


FIG.24

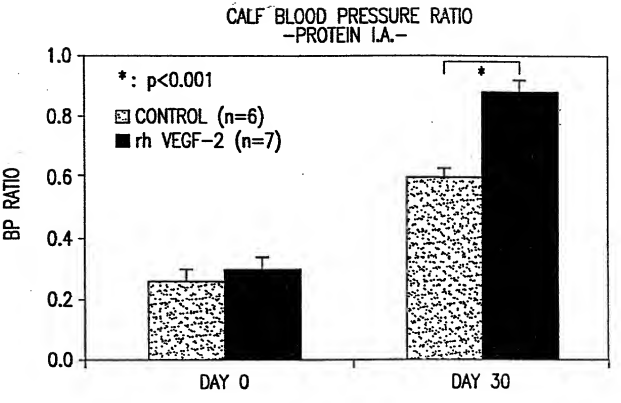


FIG.25A

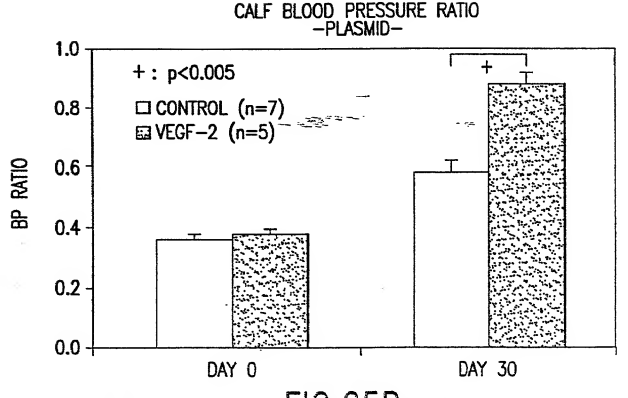


FIG.25B

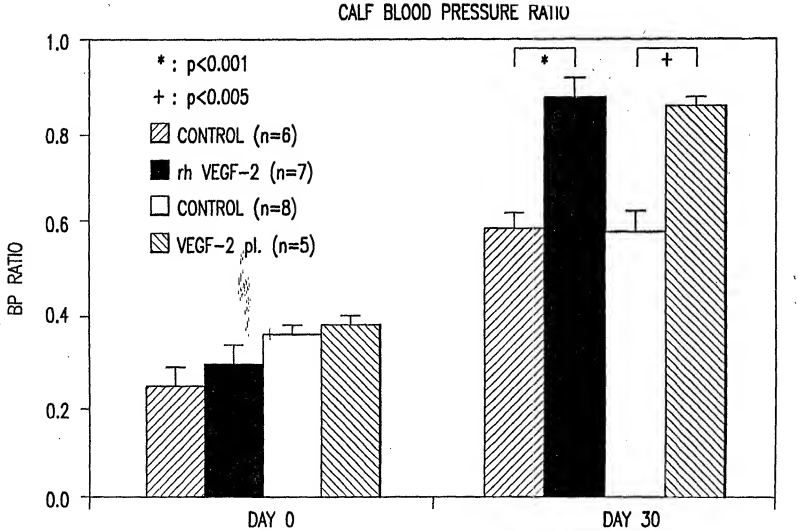


FIG.25C

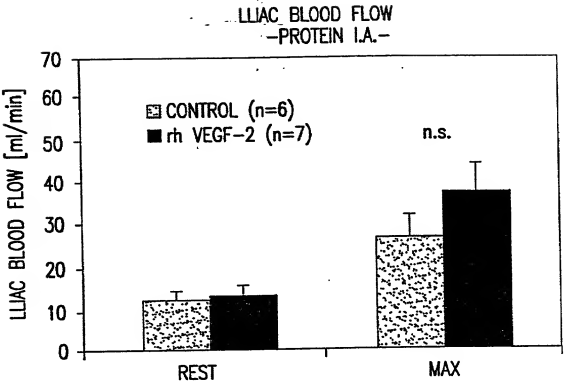


FIG.25D

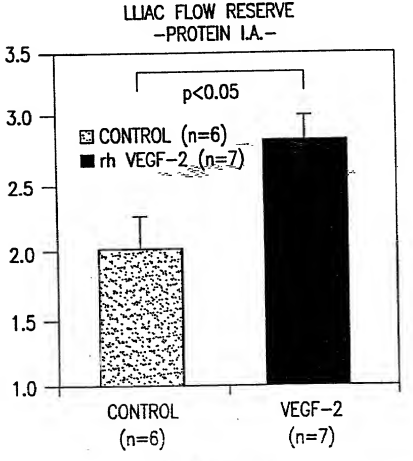


FIG.25E

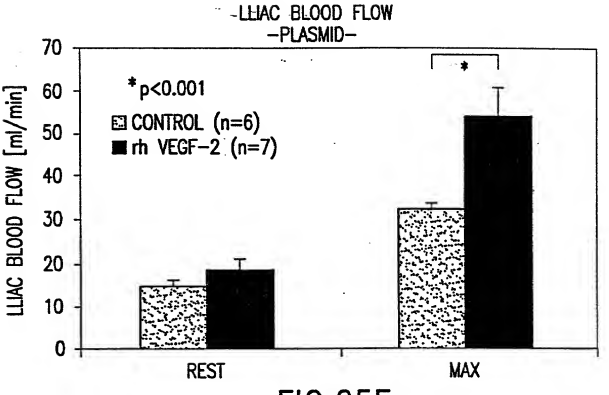


FIG.25F

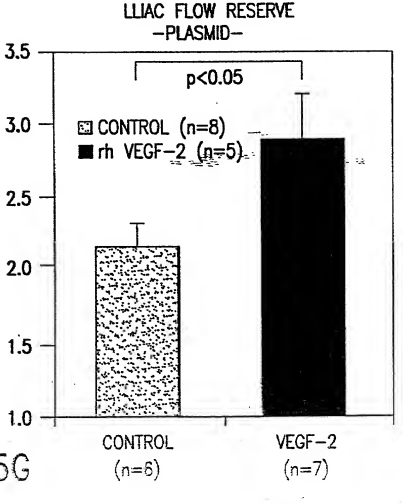


FIG.25G

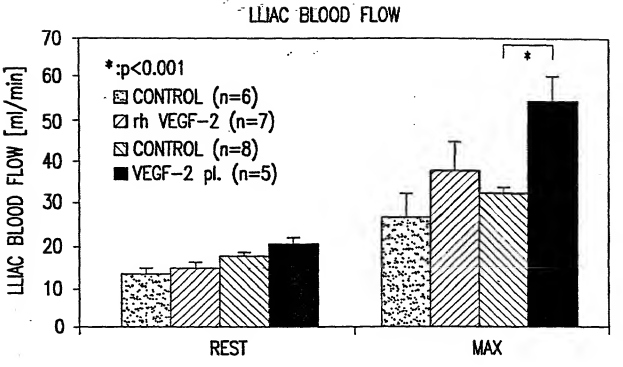


FIG.25H

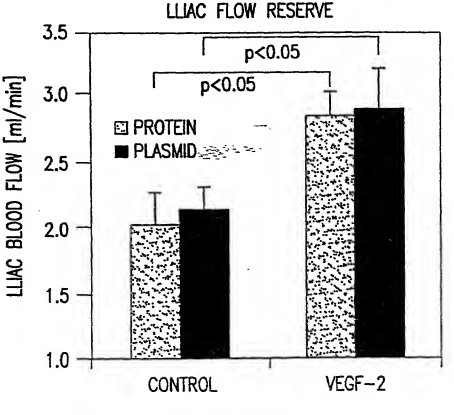


FIG.25I

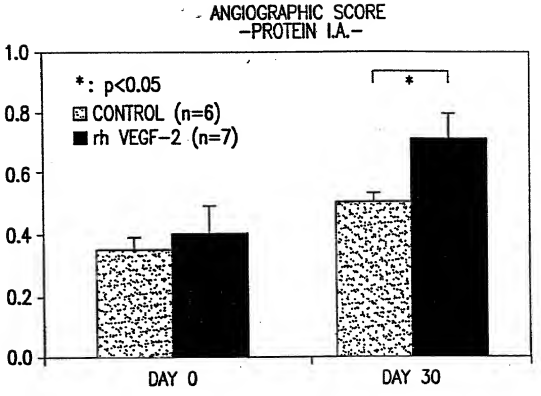


FIG.25J

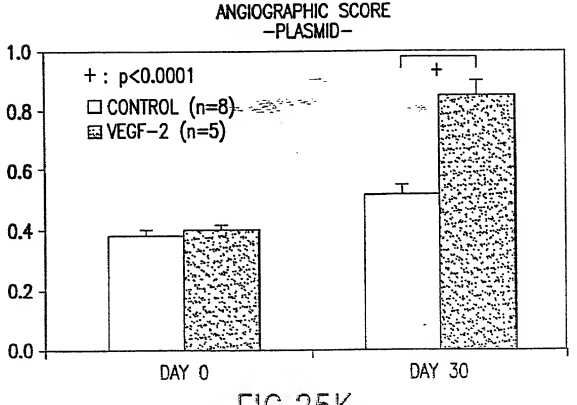


FIG.25K

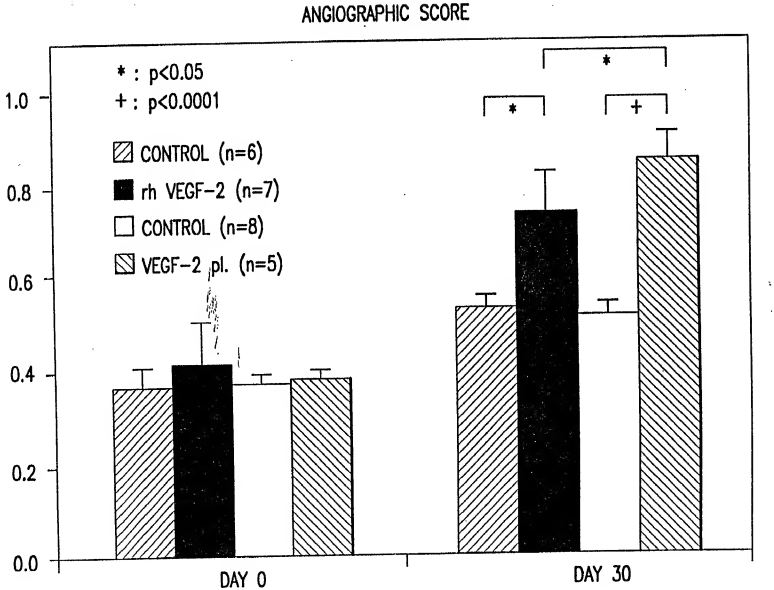


FIG.25L

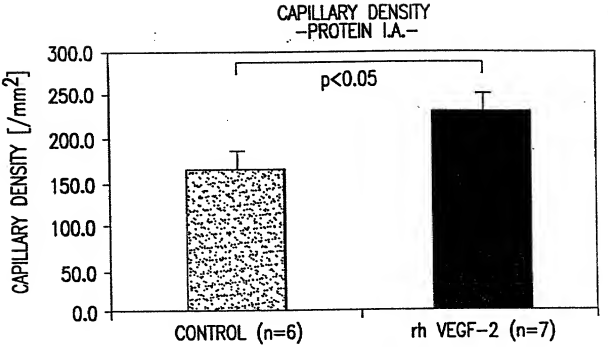


FIG.25M

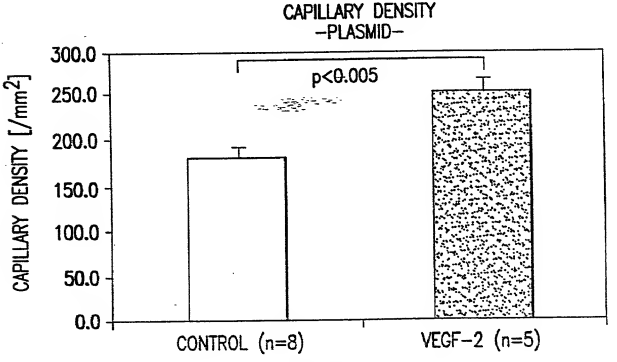


FIG.25N

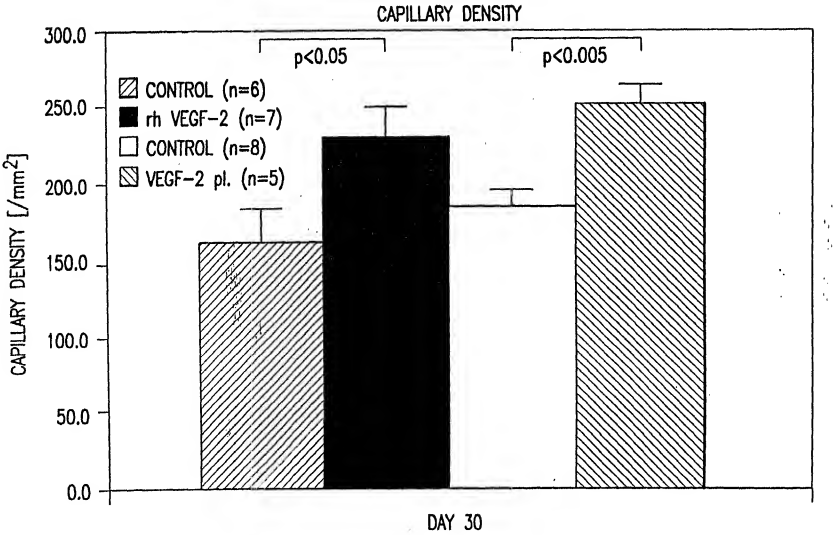


FIG.25 O

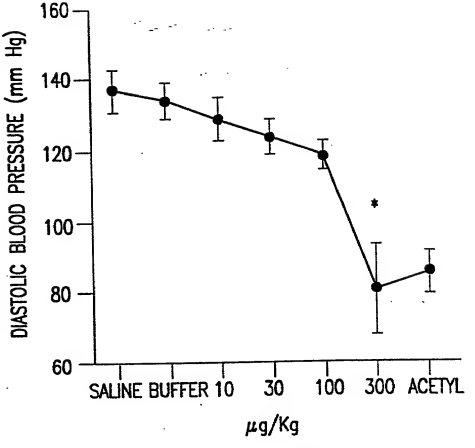


FIG.26A

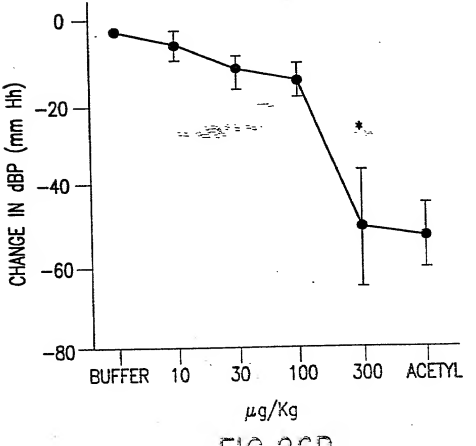


FIG.26B

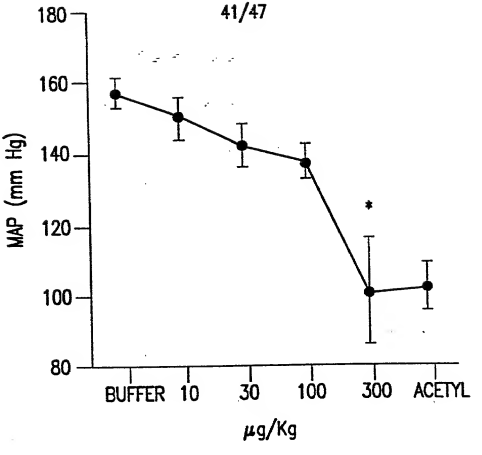


FIG.26C

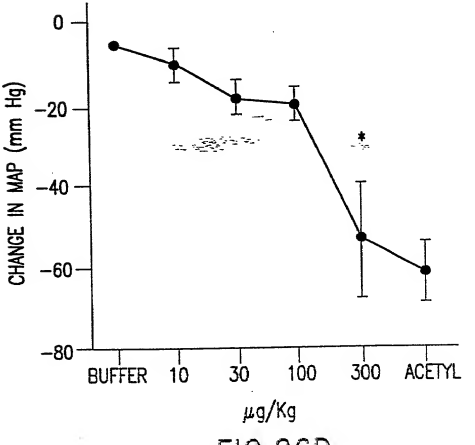


FIG.26D

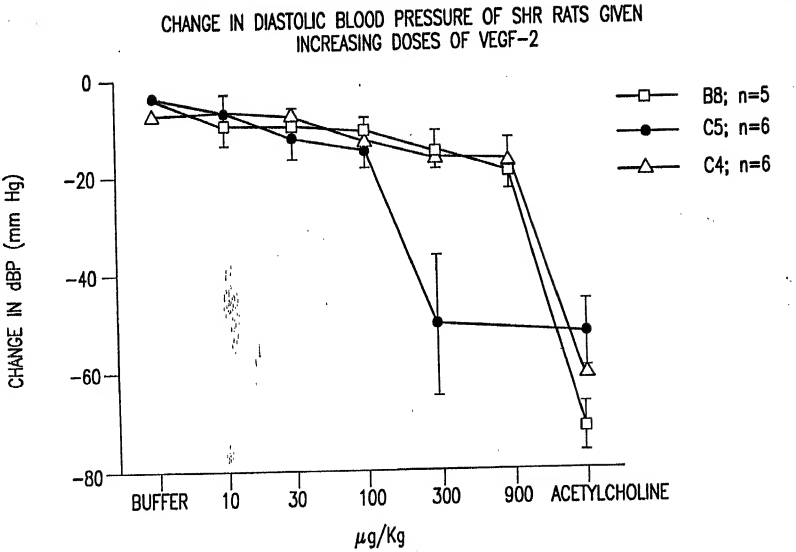


FIG.26E

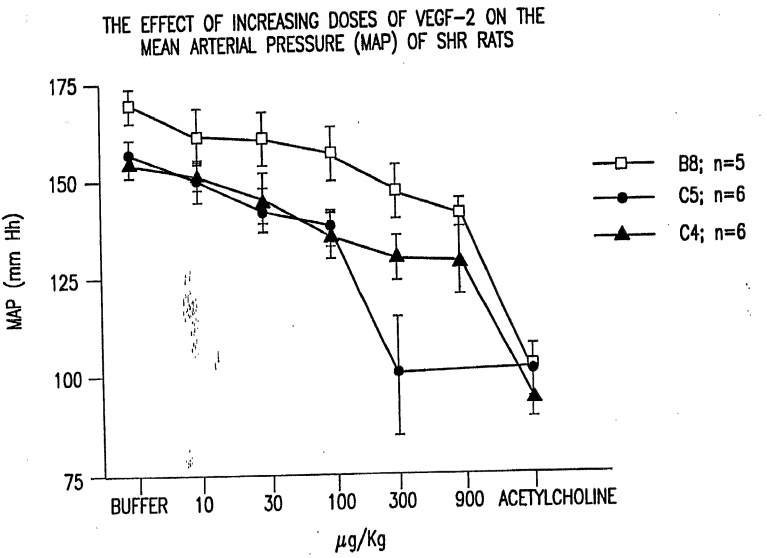


FIG.26F

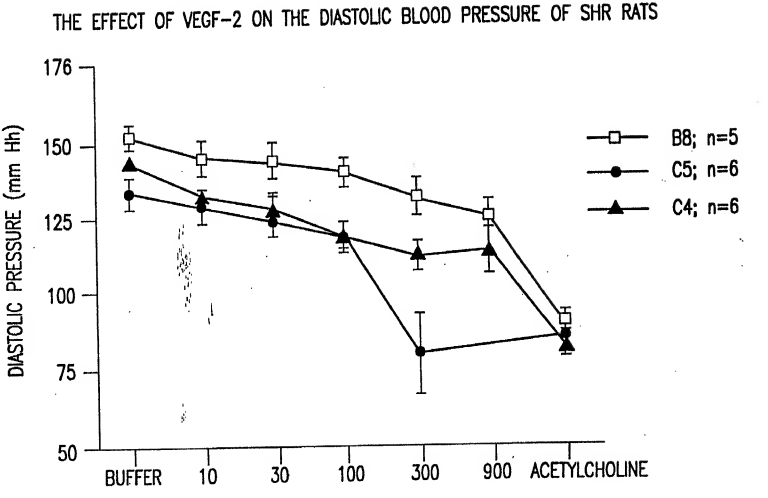


FIG.26G

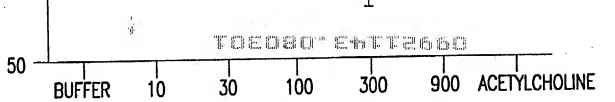


FIG.26G

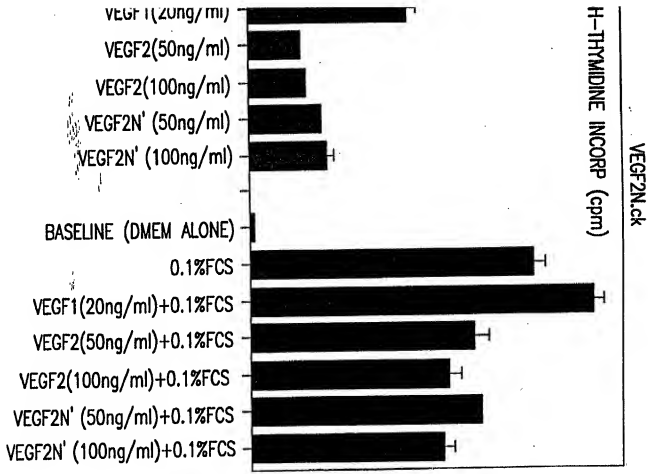


FIG.27

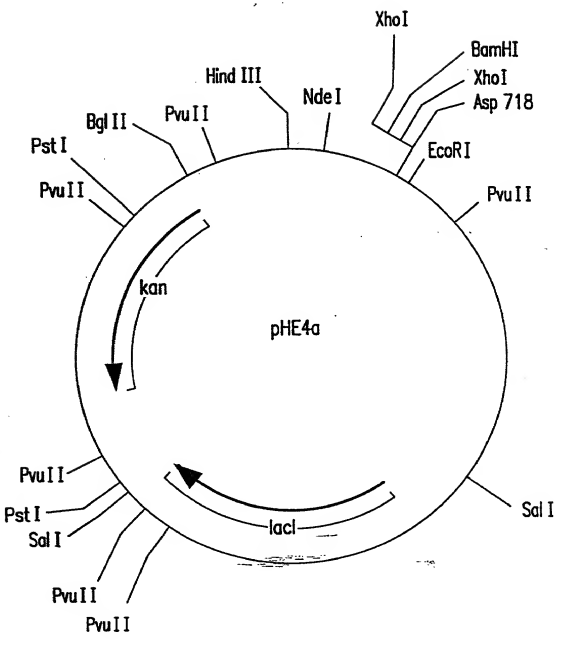

XhoI
BamHI
XhoI
Asp 718
EcoRI
PvuII
NdeI
Hind III
PvuII
BglII
PstI
PvuII
kan
pHE4a
PvuII
PstI
SalI
PvuII
PvuII
lacI
SalI

FIG.28

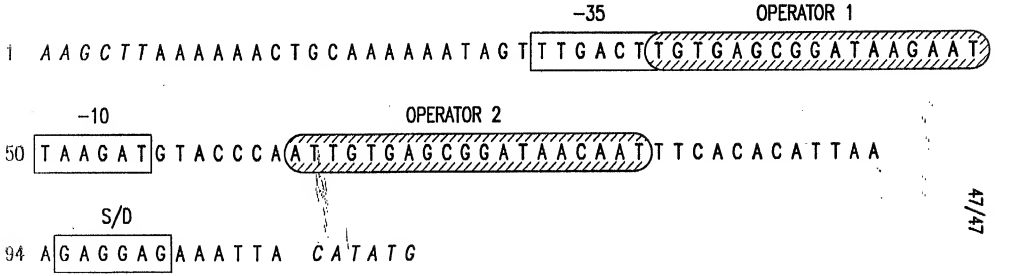


FIG.29

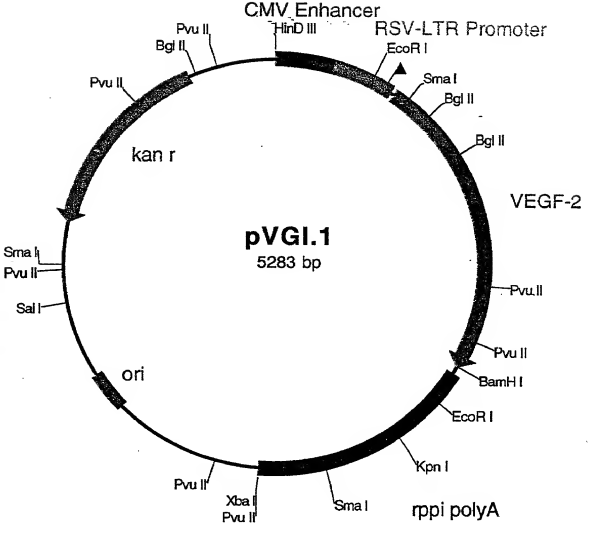

CMV Enhancer
RSV-LTR Promoter
HinD III
EcoR I
Sma I
Bgl II
Bgl II
VEGF-2
Pvu.II
Pvu II
BamH I
EcoR I
Kpn I
rppi polyA
Sma I
Pvu II
Xba I
Pvu II
ori
Sal I
Pvu II
Sma I
kan r
Pvu II
Bgl II
Pvu II
pVGI.1
5283 bp

FIG. 30

FIG. 31A

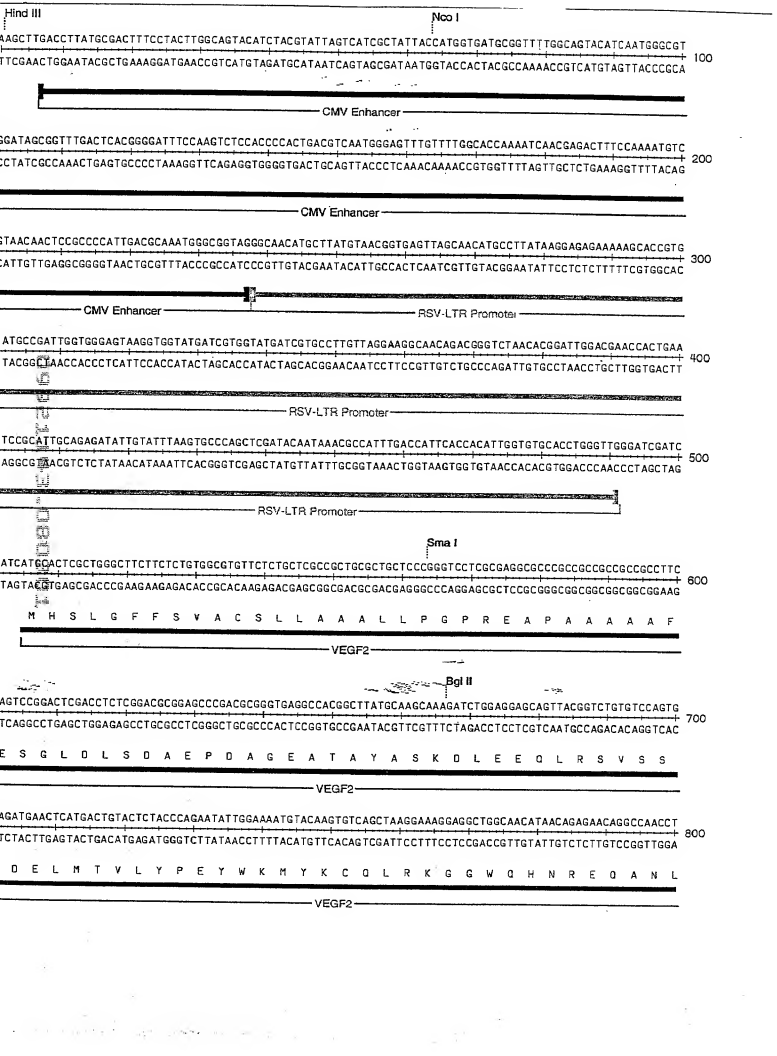

Hind III
Nco I
CMV Enhancer
CMV Enhancer
CMV Enhancer
RSV-LTR Promoter
RSV-LTR Promoter
RSV-LTR Promoter
Sma I
Bgl II
VEGF2
VEGF2
VEGF2
100
200
300
400
500
600
700
800

FIG. 31B

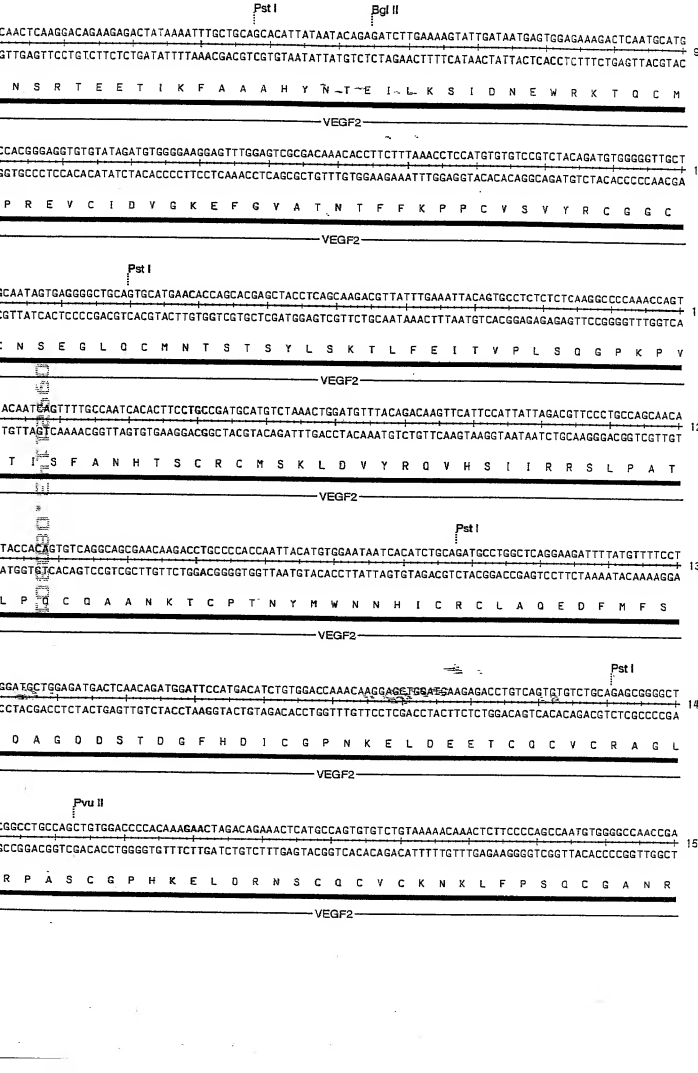

Pst I
Bgl II
CAACTCAAGGACAGAAGAGACTATAAAATTTGCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTGGAGAAAGACTCAATGCATG
GTTGAGTTCCTGTCTTCTCTGATATTTTAAACGACGTCGTGTAATATTATGTCTCTAGAACTTTTCATAACTATTACTCACCTCTTTCTGAGTTACGTAC
900
N S R T E E T I K F A A A H Y N T E I L K S I D N E W R K T Q C M
VEGF2
CCACGGGAGGTGTGTATAGATGTGGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTGTGTCCGTCTACAGATGTGGGGGTTGCT
GGTGCCCTCCACACATATCTACACCCCTTCCTCAAACCTCAGCGCTGTTTGTGGAAGAAATTTGGAGGTACACACAGGCAGATGTCTACACCCCCAACGA
1000
P R E V C I D V G K E F G V A T N T F F K P P C V S V Y R C G G C
VEGF2
Pst I
GCAATAGTGAGGGGCTGCAGTGCATGAACACCAGCACGAGCTACCTCAGCAAGACGTTATTTGAAATTACAGTGCCTCTCTCTCAAGGCCCCAAACCAGT
CGTTATCACTCCCCGACGTCACGTACTTGTGGTCGTGCTCGATGGAGTCGTTCTGCAATAAACTTTAATGTCACGGAGAGAGAGTTCCGGGGTTTGGTCA
1100
N S E G L Q C M N T S T S Y L S K T L F E I T V P L S Q G P K P V
VEGF2
ACAATCAGTTTTGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATGTTTACAGACAAGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACA
TGTTAGTCAAAACGGTTAGTGTGAAGGACGGCTACGTACAGATTTGACCTACAAATGTCTGTTCAAGTAAGGTAATAATCTGCAAGGGACGGTCGTTGT
1200
T I S F A N H T S C R C M S K L D V Y R Q V H S I I R R S L P A T
VEGF2
Pst I
TACCACAGTGTCAGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCCTGGCTCAGGAAGATTTTATGTTTTCCT
ATGGTGTCACAGTCCGTCGCTTGTTCTGGACGGGGTGGTTAATGTACACCTTATTAGTGTAGACGTCTACGGACCGAGTCCTTCTAAAATACAAAAGGA
1300
L P Q C Q A A N K T C P T N Y M W N N H I C R C L A Q E D F M F S
VEGF2
Pst I
GGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAGACCTGTCAGTGTGTCTGCAGAGCGGGGCT
CCTACGACCTCTACTGAGTTGTCTACCTAAGGTACTGTAGACACCTGGTTTGTTCCTCGACCTACTTCTCTGGACAGTCACACAGACGTCTCGCCCCGA
1400
D A G Q D S T D G F H D I C G P N K E L D E E T C Q C V C R A G L
VEGF2
Pvu II
CGGCCTGCCAGCTGTGGACCCCACAAAGAACTAGACAGAAACTCATGCCAGTGTGTCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGCCAACCGA
GCCGGACGGTCGACACCTGGGGTGTTTCTTGATCTGTCTTTGAGTACGGTCACACAGACATTTTTGTTTGAGAAGGGGTCGGTTACACCCCGGTTGGCT
1500
R P A S C G P H K E L D R N S C Q C V C K N K L F P S Q C G A N R
VEGF2

FIG. 31C

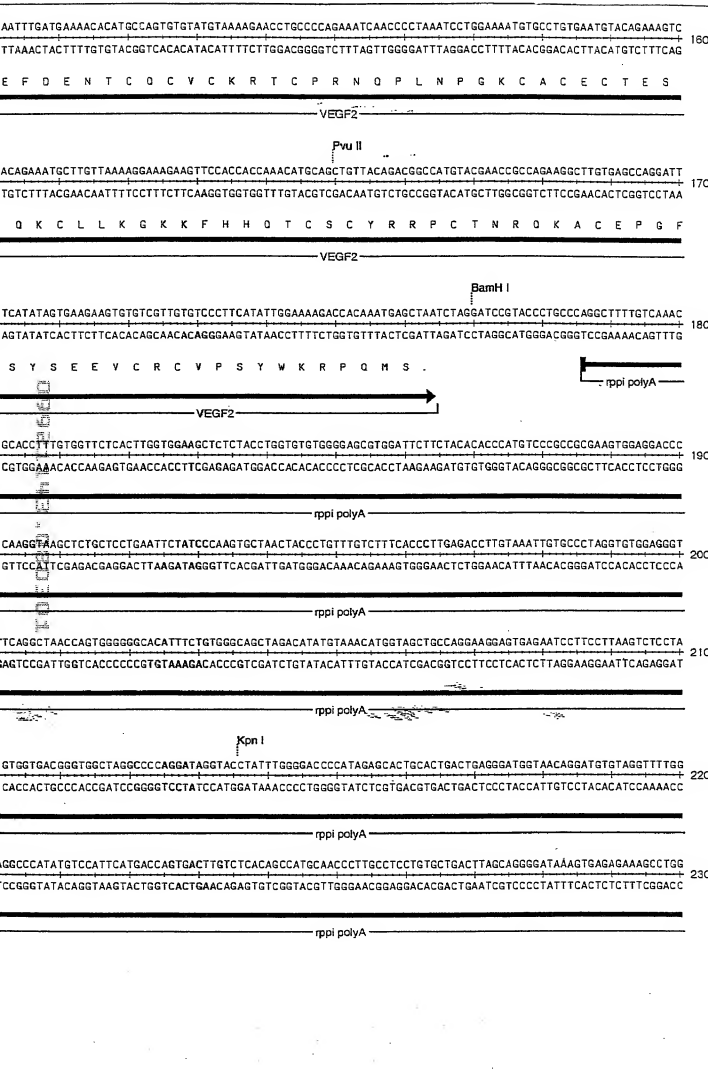

AATTTGATGAAAACACATGCCAGTGTGTATGTAAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAAAATGTGCCTGTGAATGTACAGAAAGTC
TTAAACTACTTTTGTGTACGGTCACACATACATTTTCTTGGACGGGGTCTTTAGTTGGGGATTTAGGACCTTTTACACGGACACTTACATGTCTTTCAG
1600
E F D E N T C Q C V C K R T C P R N Q P L N P G K C A C E C T E S
VEGF2
Pvu II
ACAGAAATGCTTGTTAAAAGGAAAGAAGTTCCACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAGAAGGCTTGTGAGCCAGGATT
TGTCTTTACGAACAATTTTCCTTTCTTCAAGGTGGTGGTTTGTACGTCGACAATGTCTGCCGGTACATGCTTGGCGGTCTTCCGAACACTCGGTCCTAA
1700
Q K C L L K G K K F H H Q T C S C Y R R P C T N R Q K A C E P G F
VEGF2
BamH I
TCATATAGTGAAGAAGTGTGTCGTTGTGTCCCTTCATATTGGAAAAGACCACAAATGAGCTAATCTAGGATCCGTACCCTGCCCAGGCTTTTGTCAAAC
AGTATATCACTTCTTCACACAGCAACACGGGAAGTATAACCTTTTCTGGTGTTTACTCGATTAGATCCTAGGCATGGGACGGGTCCGAAAACAGTTTG
1800
S Y S E E V C R C V P S Y W K R P Q M S .
rppi polyA
VEGF2
GCACCTTTGTGGTTCTCACTTGGTGGAAGCTCTCTACCTGGTGTGTGGGGAGCGTGGATTCTTCTACACACCCATGTCCCGCCGCGAAGTGGAGGACCC
CGTGGAAACACCAAGAGTGAACCACCTTCGAGAGATGGACCACACACCCCTCGCACCTAAGAAGATGTGTGGGTACAGGGCGGCGCTTCACCTCCTGGG
1900
rppi polyA
CAAGGTAAGCTCTGCTCCTGAATTCTATCCCAAGTGCTAACTACCCTGTTTGTCTTTCACCCTTGAGACCTTGTAAATTGTGCCCTAGGTGTGGAGGGT
GTTCCATTCGAGACGAGGACTTAAGATAGGGTTCACGATTGATGGGACAAACAGAAAGTGGGAACTCTGGAACATTTAACACGGGATCCACACCTCCCA
2000
rppi polyA
TCAGGCTAACCAGTGGGGGGCACATTTCTGTGGGCAGCTAGACATATGTAAACATGGTAGCTGCCAGGAAGGAGTGAGAATCCTTCCTTAAGTCTCCTA
GAGTCCGATTGGTCACCCCCCGTGTAAAGACACCCGTCGATCTGTATACATTTGTACCATCGACGGTCCTTCCTCACTCTTAGGAAGGAATTCAGAGGAT
2100
rppi polyA
Xpn I
GTGGTGACGGGTGGCTAGGCCCAGGATAGGTACCTATTTGGGGACCCCATAGAGCACTGCACTGACTGAGGGATGGTAACAGGATGTGTAGGTTTTGG
CACCACTGCCCACCGATCCGGGGTCCTATCCATGGATAAACCCCTGGGGTATCTCGTGACGTGACTGACTCCCTACCATTGTCCTACACATCCAAAACC
2200
rppi polyA
AGGCCCATATGTCCATTCATGACCAGTGACTTGTCTCACAGCCATGCAACCCTTGCCTCCTGTGCTGACTTAGCAGGGGATAAAGTGAGAGAAAGCCTGG
TCCGGGTATACAGGTAAGTACTGGTCACTGAACAGAGTGTCGGTACGTTGGGAACGGAGGACACGACTGAATCGTCCCCTATTTCACTCTCTTTCGGACC
2300
rppi polyA

FIG. 31D

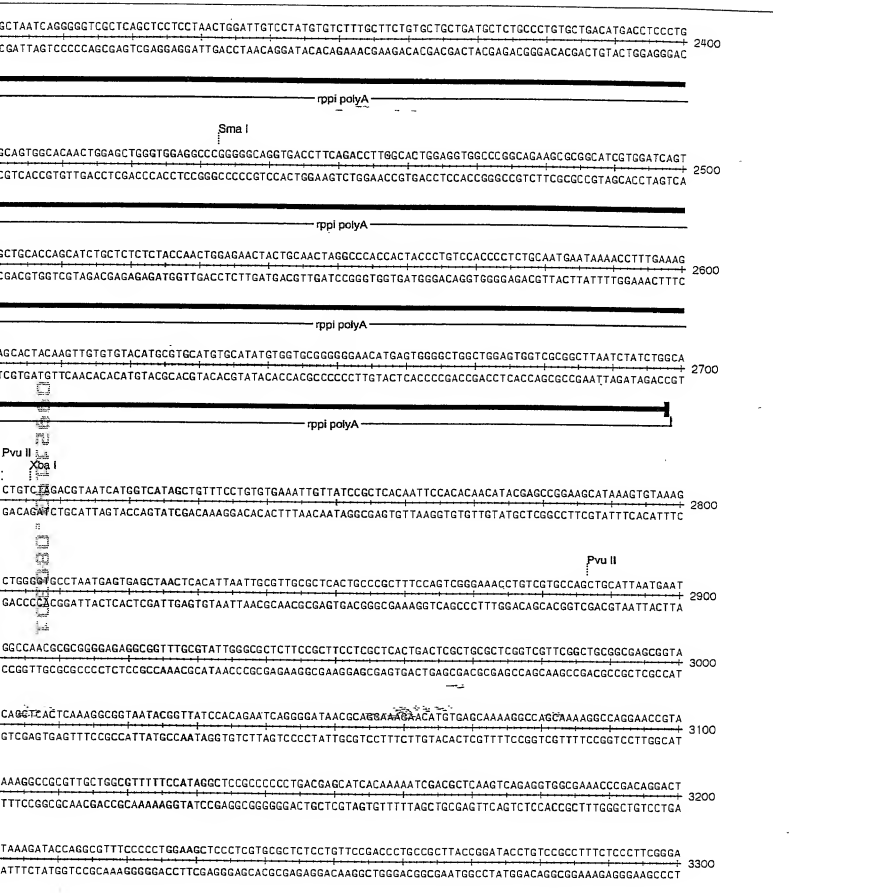

rppi polyA
Sma I
rppi polyA
rppi polyA
rppi polyA
Pvu II
Xba I
Pvu II
2400
2500
2600
2700
2800
2900
3000
3100
3200
3300

FIG. 31E

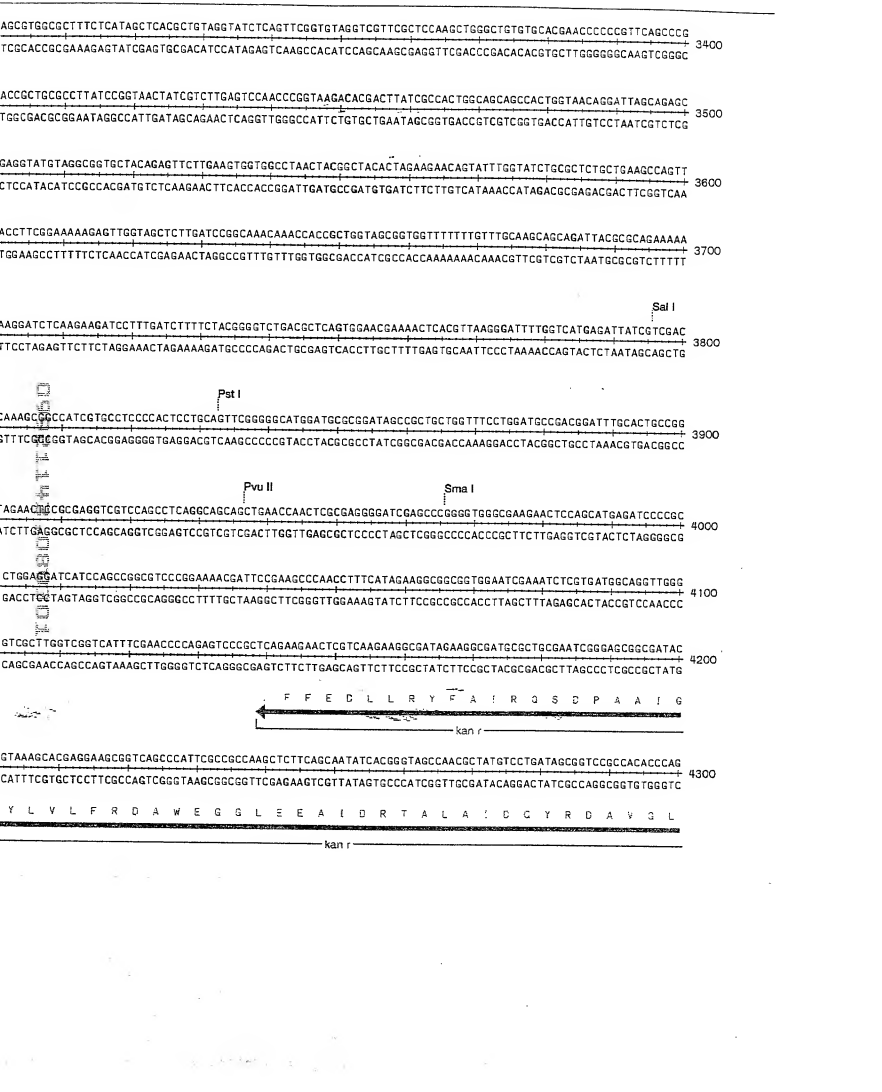

3400
3500
3600
3700
Sal I
3800
Pst I
3900
Pvu II
Sma I
4000
4100
4200
F F E D L L R Y F A I R Q S D P A A I G
kan r
4300
Y L V L F R D A W E G G L E E A I D R T A L A I D G Y R D A V G L
kan r

FIG. 31F

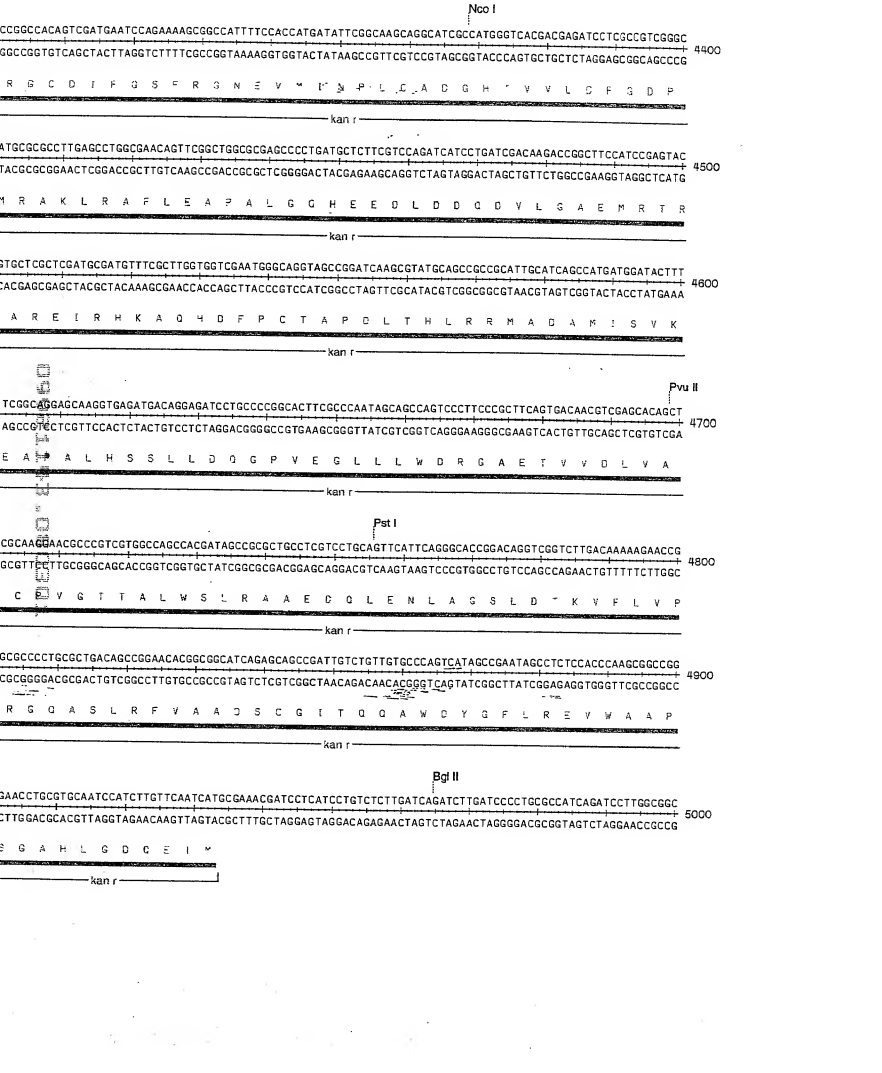

Nco I
4400
kan r
4500
kan r
4600
kan r
Pvu II
4700
kan r
Pst I
4800
kan r
4900
kan r
Bgl II
5000
kan r

FIG. 31 G

Pvu II

```
AAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGT
---------------------------------------------------------------------------------------------------- 5100
TTCTTTCGGTAGGTCAAATGAAACGTCCCGAAGGGTTGGAATGGTCTCCCGCGGGGTCGACCGTTAAGGCCAAGCGAACGACAGGTATTTTGGCGGGTCA

CTAGCTATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGCGTTTTCCCTTGTCCAGATAGCCCAGTAGCTGACATTCATCCGGGG
---------------------------------------------------------------------------------------------------- 5200
GATCGATAGCGGTACATTCGGGTGACGTTCGATGGACGAAAGAGAAACGCGAACGCAAAAGGGAACAGGTCTATCGGGTCATCGACTGTAAGTAGGCCCC

TCAGCACCGTTTCTGCGGACTGGCTTTCTACGTGTTCCGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG
----------------------------------------------------------------------------------> 5283
AGTCGTGGCAAAGACGCCTGACCGAAAGATGCACAAGGCGAAGGAAATCGTCGGGAACGCGGGACTCACGAACGCCGTCGCAC
```